



PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search **Protein** for

Limits Preview/Index History Clipboard Details

Display **GenPept** Show **5** Send to

Range: from **begin** to **end** Features: ☐ SNP ☐ CDD ☒ MGC ☒ HPRD ☒ !

1: CAF33259. Reports unnamed protein p...[gi:45112868]

[BLink](#), [Links](#)

LOCUS CAF33259 325 aa linear PLN 04-MAR-2004
 DEFINITION unnamed protein product [Penicillium citrinum].
 ACCESSION CAF33259
 VERSION CAF33259.1 GI:45112868
 DBSOURCE embl accession [CQ769141.1](#)
 KEYWORDS .
 SOURCE Penicillium citrinum
 ORGANISM [Penicillium citrinum](#)
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
 REFERENCE 1
 AUTHORS Asako,H. and Shimizu,M.
 TITLE Modified reductase and its gene and use thereof
 JOURNAL Patent: EP 1386961-A 04-FEB-2004;
 Sumitomo Chemical Company, Limited (JP)
 FEATURES
 source Location/Qualifiers
 1..325
 /organism="Penicillium citrinum"
 /db_xref="taxon:5077"
Protein 1..325
 /name="unnamed protein product"
CDS 1..325
 /coded_by="CQ769141.1:1..978"

ORIGIN

```

1 msngktftls ngvkipgvvf gtfasegskg etytavttal ktgyrhldca wylnegevg
61 egirdflken psvkredifv ctkvwnhlhr yedvlwsidd slkrlgldyv dmflvhwpia
121 aekngqgepk igpdgkyvil kdltenept wramekiyed rkarsigvsn wtiadlekms
181 kfakvmphan qieihpflpn eelvqycfsk nimpvayspl gsqnqvpttg ervsenktln
241 eiaekgntln aqvliawglr rgyvvpkss npkriesnfk sielsdadfe ainavakgrh
301 frfvnmkdtf gydvwpeeta knlsa

```

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Dec 8 2005 13:13:13



PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search for

Limits Preview/index History Clipboard Details

Display Show Range: from to ☐ Reverse complemented strand Features: ☐☐ 1: [CQ769141](#). Reports Sequence 2 from P...[gi:45112867][Links](#)

LOCUS CQ769141 978 bp DNA linear PAT 04-MAR-2004

DEFINITION Sequence 2 from Patent EP1386961.

ACCESSION CQ769141

VERSION CQ769141.1 GI:45112867

KEYWORDS .

SOURCE *Penicillium citrinum*ORGANISM *Penicillium citrinum*Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; *Penicillium*.

REFERENCE 1

AUTHORS Asako,H. and Shimizu,M.

TITLE Modified reductase and its gene and use thereof .

JOURNAL Patent: EP 1386961-A 2 04-FEB-2004;
Sumitomo Chemical Company, Limited (JP)

FEATURES

source Location/Qualifiers

1..978

/organism="Penicillium citrinum"

/mol_type="unassigned DNA"

/db_xref="taxon:5077"

CDS

1..978

/note="unnamed protein product"

/codon_start=1

/protein_id="CAF33259.1"

/db_xref="GI:45112868"

/translation="MSNGKTFTLNSGVKIPGVGFGTFASEGSKGETYTAVTALKTGY
RHLDCAWYYLNEGEVGEIGIRDFLKENPSVKREDIFVCTKVWNHLHRYEDVLWSIDDSL
KRLGLDYVDMFLVHWPIAAEKNGQGEPKIGPDGKYVILKDLTENPEPTWRAMEKIYED
RKARSIGVSNWTIADLEKMSKFAKVMPHANQIEIHPFLPNEELVQYCFSKNIMPVAYS
PLGSQNQVPTTGERVSENKTLNEIAEKGGNTLAQVLIAGLRRGVVLPKSSNPKRIE
SNFKSIELSDADFEAINAVAKGRHFRFVNMKDTFGYDVWPEETAKNLSA"

ORIGIN

```
1 atgtctaacg gaaagacttt cacattgagc aacggcggtca agattcctgg cgctcggtttt
61 ggtaccttcg ctagtgaagg ttccaagggc gagacctata ctgctgtcac cactgccctg
121 aagaccggtt accgtcactt ggactgtgcc tggactacc tgaacgaggg tgaggttggt
181 gagggtatcc gtgacttcct gaaggagaac ccctcgggtga agcgtgagga catcttcgtc
241 tgcaccaagg tgtggaacca cctccaccgt tatgaggacg tcctctggtc cattgacgac
301 tccctgaagc gtcttgact tgactacgtt gatatgttcc tcgttcactg gccattgct
361 gccgagaaga atggccaggg tgagcccaag attggccctg acggcaaata cgtcattctc
421 aaggacctga ccgagaaccc cgagcccaaca tggcgcgcta tggagaagat ttatgaggat
481 cgcaaggcca ggtccattgg tgtctccaac tggaccattg ccgacctga gaagatgtcc
541 aagttcgcca aggtcatgcc tcacgccaac cagatcgaga ttcacccctt cctgccaac
601 gaggagctgg tgcagtactg cttctccaag aacattatgc ccgtggccta ctctcctctg
661 ggctcgaga accaggttcc caccaccggt gagcgggtca gcgagaacaa gactctgaac
721 gagatcgccg agaagggcgg caacaccctt gctcaggttc ttattgcctg gggctgcgc
781 cgtggctacg tcgttctccc caagagctcc aacccaagc gcattgagtc caacttcaag
```

```
841 agcattgagc tctccgatgc cgactttgaa gccatcaatg ccgttgccaa gggtcgtcac
901 ttccgtttcg tcaacatgaa ggatactttc ggatatgatg tctggcccga ggagaccgcc
961 aagaacctgt ctgctga
```

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Dec 8 2005 13:13:13

Database : UniProt_05.80:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1514	87.5	325	2	Q877A2_ASPOR	Q877a2 aspergillus
2	1477	85.3	325	2	Q4WQ65_ASPFU	Q4wq65 aspergillus
3	1471	85.0	325	2	Q5B1L7_EMENI	Q5b1l7 aspergillus
4	1471	85.0	325	2	Q7Z8L1_EMENI	Q7z8l1 emericella
5	1205.5	69.6	331	2	Q7S3U4_NEUCR	Q7s3u4 neurospora
6	1191	68.8	327	2	Q6RZX1_TRIAT	Q6rzx1 trichoderma
7	1137.5	65.7	323	2	Q51QM9_MAGGR	Q51qm9 magnaporthe
8	1038	60.0	256	2	Q4I4F0_GIBZE	Q4i4f0 gibberella
9	1037	59.9	254	2	O74646_GIBZE	O74646 gibberella
10	635	36.7	355	2	Q4PHK0_USTMA	Q4phk0 ustilago ma
11	623	36.0	1224	2	Q4P7C0_USTMA	Q4p7c0 ustilago ma
12	602.5	34.8	332	2	Q4IEY5_GIBZE	Q4iey5 gibberella
13	595.5	34.4	309	2	Q55SW0_CRYNE	Q55sw0 cryptococcu
14	593.5	34.3	309	2	Q5KH94_CRYNE	Q5kh94 cryptococcu
15	583	33.7	310	2	Q6FR42_CANGA	Q6fr42 candida gla
16	575.5	33.2	310	2	Q6FY54_CANGA	Q6fy54 candida gla
17	574.5	33.2	312	1	GCY_YEAST	P14065 saccharomyc
18	570.5	33.0	309	2	Q6CRC8_KLULA	Q6crc8 kluyveromyc
19	568	32.8	321	1	YDG7_SCHPO	Q10494 schizosacch
20	565.5	32.7	325	2	Q5KLM8_CRYNE	Q5klm8 cryptococcu
21	563.5	32.6	325	2	Q55YB1_CRYNE	Q55yb1 cryptococcu
22	560.5	32.4	313	2	Q4X1E8_ASPFU	Q4x1e8 aspergillus
23	559.5	32.3	322	1	ALDX_SPOSA	P27800 sporobolomy
24	559	32.3	314	2	Q5B0E4_EMENI	Q5b0e4 aspergillus

Database : A_Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1731	100.0	325	5	ABB77965	Abb77965 Protein w
2	1731	100.0	325	7	ADE39629	Ade39629 Penicilli
3	1731	100.0	325	8	ADH44214	Adh44214 Penicilli
4	1731	100.0	325	8	ADL18258	Adl18258 Penicilli
5	1731	100.0	325	8	ADK70247	Adk70247 Penicilli
6	1731	100.0	325	8	ADM46686	Adm46686 325 amino
7	1731	100.0	325	8	ADM46567	Adm46567 Penicilli
8	1731	100.0	325	8	ADK51190	Adk51190 Wild-type
9	1731	100.0	325	8	ADN97092	Adn97092 3 hydroxy
10	1728	99.8	325	8	ADK51203	Adk51203 Mutant Pe
11	1726	99.7	325	8	ADK51204	Adk51204 Mutant Pe
12	1723	99.5	325	8	ADK51205	Adk51205 Mutant Pe
13	972.5	56.2	255	8	ADN20743	Adn20743 Bacterial
14	575.5	33.2	312	2	AAW29220	Aaw29220 S. cerevi
15	574.5	33.2	312	2	AAW29217	Aaw29217 S. cerevi
16	574.5	33.2	312	4	AAG63565	Aag63565 Amino aci
17	574.5	33.2	312	5	ABG93198	Abg93198 S. cerevi
18	574.5	33.2	312	8	ADS43942	Ads43942 Bacterial
19	574.5	33.2	313	4	AAG63566	Aag63566 Synthetic
20	573.5	33.1	312	2	AAW29218	Aaw29218 S. cerevi
21	568	32.8	321	8	ADN19632	Adn19632 Bacterial

*Not all
same in every
pen
had data*

US-10-004-115B-1

parental DNA em si
no variant

[illegible]

Db

301 FRFVNMKDTFGYDVWPEETAKNLSA 325

Database : PIR_80:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	574.5	33.2		312	1	S22846	probable aldehyde
2	568	32.8		321	2	T38413	probable oxidoredu
3	559.5	32.3		323	2	S78113	aldehyde reductase
4	555	32.1		312	2	S61163	aldo-keto reductas
5	553	31.9		327	1	S76143	probable aldehyde
6	548.5	31.7		325	2	T39169	probable oxidoredu
7	547.5	31.6		344	1	S46020	probable aldehyde
8	529.5	30.6		309	2	A84599	hypothetical prote
9	529	30.6		290	2	T02543	aldehyde dehydroge
10	527.5	30.5		309	2	B84599	hypothetical prote
11	523.5	30.2		294	2	T02542	probable alcohol d
12	523.5	30.2		313	2	T09670	abscisic acid acti
13	521	30.1		320	2	T48188	aldose reductase-1
14	516	29.8		280	2	C98038	conserved hypothet
15	516	29.8		280	2	C95172	oxidoreductase, al
16	509	29.4		316	2	A37990	aldose reductase h
17	508.5	29.4		281	2	D86658	oxidoreductase ycg
18	503	29.1		276	2	C70040	plant-metabolite d
19	501.5	29.0		310	2	T17013	D-sorbitol-6-phosp
20	500	28.9		280	2	D69988	plant metabolite d
21	499.5	28.9		316	1	A60603	aldehyde reductase